## Raw Sequence Listing Error Summary

	ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/22/,68
ATTN:	: NEW RULES CASES: PI	LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WH	
1	Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.		
	• • • • • • • • • • • • • • • • • • • •	This may occur if your file was retrieved in a word processor after creating it.	
		Please adjust your right margin to .3, as this will prevent "	
2	Wrapped Aminos	The amino acid number/text at the end of each line "wrapp	ed " down to the next line
		This may occur if your file was retrieved in a word process	
		Please adjust your right margin to .3, as this will prevent "	
3	Incorrect Line Length	The rules require that a line not exceed 72 characters in le	ngth. This includes spaces.
4	Misaligned Amino Acid	The numbering under each 5th amino acid is misaligned.	This may be caused by the use of tabs
	Numbering	between the numbering. It is recommended to delete any to	
5	Non-ASCII	This file was not saved in ASCII (DOS) text, as required by	y the Sequence Rules.
		Please ensure your subsequent submission is saved in AS	CII text so that it can be processed.
6	Variable Length	Sequence(s) contain n's or Xaa's which represented	more than one residue.
		As per the rules, each n or Xaa can only represent a single	residue.
		Please present the maximum number of each residue having	ng variable length and
		indicate in the (ix) feature section that some may be missing	ng.
7	Patentin ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<22	
		sequence(s) Normally, Patentin would au	tomatically generate this section from the
		previously coded nucleic acid sequence. Please manually to the subsequent amino acid sequence.	copy the relevant <220>-<223> section
8	Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please use the fo (2) INFORMATION FOR SEQ ID NO:X:	ollowing format for each skipped sequence:
	` ,	(i) SEQUENCE CHARACTERISTICS:(Do not insert any h	eadings under "SEQUENCE CHARACTERISTICS")
		(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:	·
		This sequence is intentionally skipped	
		Please also adjust the "(iii) NUMBER OF SEQUENCES:"	response to include the skipped sequence(s).
	Skipped Sequences	Sequence(s) missing. If intentional, please use the fo	llowing format for each skipped sequence.
	(NEW RULES)	<210> sequence id number	
		<400> sequence id number 000	
10	Use of n's or Xaa's	Use of n's and/or Xaa's have been detected in the Sequence	o Listing
	(NEW RULES)	Use of <220> to <223> is MANDATORY if n's or Xaa's are	•
	,	In <220> to <223> section, please explain location of n or X	•
11	Use of <213>Organism	Sequence(s) are missing this mandatory field or it	s response.
	(NEW RULES)		·
12 🗸	Use of <220>Feature >	Sequence(s) are missing the <220>Feature and asso	cisted headings
	/	Use of <220> to <223> is MANDATORY if <213>ORGANI	
	,	Please explain source of genetic material in <220> to <	
		(See "Federal Register," 6/01/98, Vol. 63, No.	
13	Patentin ver. 2.0 "bug"	Please do not use "Copy to Disk" function of Patentin	version 2.0. This causes a corrupted
		file, resulting in missing mandatory numeric identifiers and r	
		Instead, please use "File Manager" or any other means to co	

16 179 16

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## RAW SEQUENCE LISTING

PATENT APPLICATION US/09/227,687A

DATE: 07/19/2000

TIME: 16:34:58

Input Set: I227687A.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

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           Connelly, Gene
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           Gallant, Paul L.
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93

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PATENT APPLICATION US/09/227,687A TIME: 16:34:58

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## VERIFICATION SUMMAR PATENT APPLICATION US/09/227,687A

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Input Set: 1227687A.RAW

Line ? Error/Warning

Original Text